NCBI   Nucleotide

PubMed   Nucleotide   Protein   Genome   Structure   PopSet   Taxonomy   OMIM

Search Nucleotide ▣ for [   ]

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☐ **1: AF033348. Homo sapiens pota...[gi:2801451]**

```
LOCUS       AF033348                3232 bp   mRNA    linear   PRI 21-JAN-1998
DEFINITION  Homo sapiens potassium channel (KCNQ2) mRNA, complete cds.
ACCESSION   AF033348
VERSION     AF033348.1  GI:2801451
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3232)
  AUTHORS   Singh,N.A., Charlier,C., Stauffer,D., DuPont,B.R., Leach,R.J.,
            Melis,R., Ronen,G.M., Bjerre,I., Quattlebaum,T., Murphy,J.V.,
            McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and
            Leppert,M.
  TITLE     A novel potassium channel gene, KCNQ2, is mutated in an inherited
            epilepsy of newborns
  JOURNAL   Nat. Genet. 18 (1), 25-29 (1998)
  MEDLINE   98085864
   PUBMED   9425895
REFERENCE   2  (bases 1 to 3232)
  AUTHORS   Singh,N.A., Charlier,C., Stauffer,D., DuPont,B.R., Leach,R.J.,
            Melis,R., Ronen,R.M., Bjerre,I., Quattlebaum,T., Murphy,J.V.,
            McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and
            Leppert,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-NOV-1997) Human Genetics, University of Utah, 2030E
            15N Room 2100, Salt Lake City, UT 84112, USA
FEATURES             Location/Qualifiers
     source          1..3232
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                     /db_xref="taxon:9606"
                     /chromosome="20"
                     /map="20q13.3"
     gene            1..3232
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     CDS             128..2746
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                     /note="KvEBN1"
                     /codon_start=1
                     /product="potassium channel"
                     /protein_id="AAB97315.1"
                     /db_xref="GI:2801452"
                     /translation="MVQKSRNGGVYPGPSGEKKLKVGFVGLDPGAPDSTRDGALLIAG
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                     VFSCLVLSVFSTIKEYEKSSEGALYILEIVTIVVFGVEYFVRIWAAGCCCRYRGWRGR
                     LKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSALRSLRFLQILRMIRMDRRGGTW
                     KLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGENDHFDTYADALWWGLITLT
                     TIGYGDKYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQEQHRQKHFEKRRN
                     PAAGLIQSAWRFXATNLSRTDLHSTWQYYERTVTVPMYSSQTQTYGASRLIPPLNQLE
                     LLRNLKSKSGLAFRKDPPPEPSPSKGSPCRGPLCGCCPGRSSQKVSLKDRVFSSPRGV
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```

```
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KVEKQVLSMEKKLDFLVNIYMQRMGIPPTETEAYFGAKEPEPAPPYHSPEDSREHVDR
HGCIVKIVRSSSSTGQKNFSAPPAAPPVQCPPSTSWQPCSHPRQGHGTSPVGDHGSLV
RIPPPPAHERSLSAYGGGNRASMEFLRQEDTPGCRPPEGNLRDSDTSISIPSVDHEEL
ERSFSGFSISQSKENLDALNSCYAAVAPCAKVRPYIAEGESDTDSDLCTPCGPPPRSA
TGEGPFGDVGWAGPRK*
```

BASE COUNT   576 a   1054 c   1061 g   533 t   8 others
ORIGIN
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        1 gagtgcggaa ccgccgcctc ggccatgcgg ctcccggccg gggggcctgg gctggggccc
       61 gcgccgcccc ccgcgctccg cccccgctga gcctgagccc gacccggggc gcctcccgcc
      121 aggcaccatg gtgcagaagt cgcgcaacgg cggcgtatac cccggcccga gcggggagaa
      181 gaagctgaag gtgggcttcg tggggctgga ccccggcgcg cccgactcca cccgggacgg
      241 ggcgctgctg atcgccggct ccgaggcccc caagcgcggc agcatcctca gcaaacctcg
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      541 cgtggagtac ttcgtgcgga tctgggccgc aggctgctgc tgccggtacc gtggctggag
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      781 gaagctgctg ggctctgtgg tctatgccca cagcaaggag ctggtcactg cctggtacat
      841 cggcttcctt tgtctcatcc tggcctcgtt cctggtgtac ttggcagaga agggggagaa
      901 cgaccacttt gacacctacg cggatgcact ctggtgggggc ctgatcacgc tgaccaccat
      961 tggctacggg gacaagtacc cccagacctg gaacggcagg ctccttgcgg caaccttcac
     1021 cctcatcggt gtctccttct tcgcgctgcc tgcaggcatc ttggggtctg ggtttgccct
     1081 gaaggttcag gagcagcaca ggcagaagca ctttgagaag aggcggaacc cggcagcagg
     1141 cctgatccag tcggcctgga gattctmcgc caccaacctc tcgcgcacag acctgcactc
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     1381 cagcccgtgc agagggcccc tgtgtggatg ctgccccgga cgctctagcc agaaggtcag
     1441 tttgaaagat cgtgtcttct ccagcccccg aggcgtggct gccaagggga aggggtcccc
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     1621 caagggtgcc gcgtcacggc agaactcaga agaagcaagc ctccccggag aggacattgt
     1681 ggatgacaag agctgcccct gcgagtttgt gaccgaggac ctgacccccgg gcctcaaagt
     1741 cagcatcaga gccgtgtgtg tcatgcggtt cctggtgtcc aagcggaagt tcaaggagag
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     1861 gctgtcccga attaagagcc tgcagtccag agtggaccag atcgtggggc ggggcccagc
     1921 gatcacggac aaggaccgca ccaagggccc ggccgaggcg gagctgcccg aggaccccag
     1981 catgatggga cggctcggga aggtggagaa gcaggtcttg tccatggaga agaagctgga
     2041 cttcctggtg aatatctaca tgcagcggat gggcatcccc ccgacagaga ccgaggccta
     2101 ctttgggggcc aaagagccgg agccggcgcc gccgtaccac agcccggaag acagccggga
     2161 gcatgtcgac aggcacggct gcattgtcaa gatcgtgcgc tccagcagct ccacgggcca
     2221 gaagaacttc tcggcgcccc cggccgcgcc ccctgtccag tgtccgccct ccacctcctg
     2281 gcagccacag agccacccgc gccagggcca cggcacctcc cccgtggggg accacggctc
     2341 cctggtgcgc atcccgccgc cgcctgccca cgagcggtcg ctgtccgcct acggcggggg
     2401 caaccgcgcc agcatggagt tcctgcggca ggaggacacc ccgggctgca ggccccccga
     2461 ggggaacctg cgggacagcg acacgtccat ctccatcccg tccgtggacc acgaggagct
     2521 ggagcgttcc ttcagcggct tcagcatctc ccagtccaag gagaacctgg atgctctcaa
     2581 cagctgctac gcggccgtgg cgccttgtgc caaagtcagg ccctacattg cggagggaga
     2641 gtcagacacc gactccgacc tctgtacccc gtgcgggccc ccgccacgct cggccaccgg
     2701 cgagggtccc tttggtgacg tgggctgggc cgggcccagg aagtgaggcg gcgctgggcc
     2761 agtggacccg cccgcggccc tcctcagcac ggtgcctccg aggttttgag gcgggaaccc
     2821 tctgggggccc ttttcttaca gtaactgagt gtggcgggaa gggtgggccc tggaggggcc
     2881 catgtgggct gaaggatggg ggctcctggc agtgaccttt tacaaaagtt attttccaac
     2941 aggggctgga gggctgggca gggcctgtgg ctccaggagc agcgtgcagg agcaaggctg
     3001 ccctgtccac tctgctcaag gccgcggccg acatcagccc ggtgtgaaga ggggcggagt
     3061 gatgacgggt gttgcaacct ggcaacaagc nggggggttgn ccagccganc caagggaagc
     3121 acanaaggaa gctgtnccct aagacctncc cnaaaggcgg cctgtttggt aagactgcgc
     3181 cttggtccgg tgggttccgg cagcaaaagc gggtttttgcc gcccctgtcg tg
```
//

Revised: October 24, 2001.

NCBI **Blast 2 Sequences results**

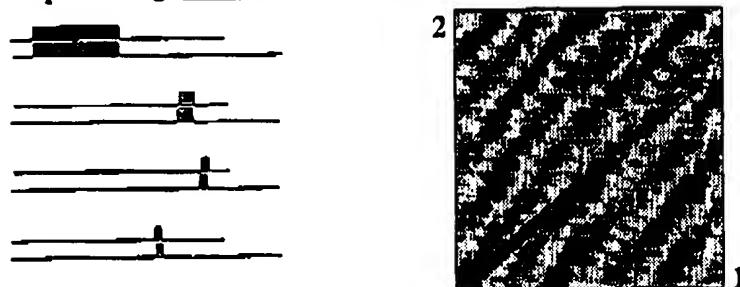PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match: [1] Mismatch: [-2] gap open: [5] gap extension: [2]

x_dropoff: [50] expect: [10.000] wordsize: [11] Filter [✓] [Align]

Sequence 1 lcl|seq_1 **Length 2088 (83 .. 2170)** = *CDS of KCNQ4*

Sequence 2 gi 2801451 **Length 2619 (128 .. 2746)** = *CDS of KCNQ2*

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score =  481 bits (250), Expect = e-132
Identities = 626/814 (76%)
 Strand = Plus / Plus
```



```
Query:            319  ctaccgccgcctgcagaactgggtctacaacgtgctggagcggccccgcggctgggcc
                       |||||||   |||||||| ;  |||||||:|||':|:|||||||| ||||||||||||
Sbjct:            346  ctaccgcaagctgcagaatttcctctacaacgtgctggagcggccgcgcggctgggcg
potassium channel  74     Y  R  K  L  Q  N  F  L  Y  N  V  L  E  R  P  R  G  W  A


Query:            379  cgtctaccacgtcttcatattttgctggtcttcagctgcctggtgctgtctgtgctg
                       | ||||||||| || | | |'  ' |||.| || |'||||  |||||||||||||| |
Sbjct:            406  catctaccacgcctacgtgttcctcctggtttttctcctgcctcgtgctgtctgtgtttt
potassium channel  94     I  Y  H  A  Y  V  F  L  L  V  F  S  C  L  V  L  S  V  F


Query:            439  cactatccaggagcaccaggaacttgccaaccagtgtctcctcatcttggaattcgtg.
                       |||  ,  :!|||| |  'I |   | ' |!   ||| 1:||  |||||  |||||
Sbjct:            466  cac atcaaggagtatgagaagagctcggaggggggccctctacatcctggaaatcgtg.
potassium channel 114     T  I  K  E  Y  E  K  S  S  E  G  A  L  Y  I  L  E  I  V


Query:            499  gatcgtggttttcggcttggagtacatcgtccgggtctggtccgccggatgctgctgc.
                       |||||||| || ||| ||||||||| |||| :|: |||||  ||||  |||| '|||||||
Sbjct:            526  tatcgtggtgttttggcgtggagtacttcgtgcggatctgggccgcaggctgctgctgc
potassium channel 134     I  V  V  F  G  V  E  Y  F  V  R  I  W  A  A  G  C  C  C
```

```
Query:          559  ctaccgaggatggcagggtcgcttccgctttgccagaaagcccttctgtgtcatcgac
                     ||||| |, ||| ||: || || ||   ||  || |||||||| | ||| :||
Sbjct:          586  gtaccgtggctggaggggggcggctcaagtttgcccggaaaccgttctgtgtgattgac
potassium channel 154    Y  R  G  W  R  G  R  L  K  F  A  R  K  P  F  C  V  I  D

Query:          619  catcgtgttcgtggcctcggtggccgtcatcgccgcgggtacccagggcaacatcttc
                     ||| |.| || ! |||i| | '| ||  : :|:'' .: ||||||||i|| ||||
Sbjct:          646  catggtgctcatcgcctccattgcggtgctggccgccggctcccagggcaacgtcttt
potassium channel 174    M  V  L  I  A  S  I  A  V  L  A  A  G  S  Q  G  N  V  F

Query:          679  cacgtccgcgctgcgcagcatgcgcttcctgcagatcctgcgcatggtgcgcatggac
                     |    :|| :|:'| |'  ||| |||||i,|||||||||||| |||||| ||| | |||||||||
Sbjct:          706  cacatctgcgctccggagcctgcgcttcctgcagattctgcggatgatccgcatggac
potassium channel 194    T  S  A  L  R  S  L  R  F  L  Q  I  L  R  M  I  R  M  D

Query:          739  ccgcggcggcacctggaagctgctgggctcagtggtctacgcgcatagcaaggagctg
                     |   ||  ||||||:.||||||||||||;||:||| |,||||||| || || ||||||||||i||
Sbjct:          766  gcggggaggcacctggaagctgctgggctctgtggtctatgcccacagcaaggagctg
potassium channel 214    R  G  G  T  W  K  L  L  G  S  V  V  Y  A  H  S  K  E  L

Query:          799  caccgcctggtacatcgggttcctggtgctcatcttcgcctccttcctggtctacctg
                     |||| ||||||||||.||'| |||||    |||||! | :|i|| ||||i||| !||| ||
Sbjct:          826  cactgcctggtacatcggcttcctttgtctcatcctggcctcgttcctggtgtacttg
potassium channel 234    T  A  W  Y  I  G  F  L  C  L  I  L  A  S  F  L  V  Y  L

Query:          859  cgagaaggacgccaactccgacttctcctcctacgccgactcgctctggtgggggacg
                     !||:!||' | ||| | |||| | ||||||':| | ||||||||||| |
Sbjct:          886  agagaagggggagaacgaccactttgacacctacgcggatgcactctggtggggcctg
potassium channel 254    E  K  G  E  N  D  H  F  D  T  Y  A  D  A  L  W  W  G  L

Query:          919  tacattgacaaccatcggctatggtgacaagacaccgcacacatggctgggcagggtc
                     | |||| ||||| i|||| .| ||||| |' || || ||| |||||| ||
Sbjct:          946  cacgctgaccaccattggctacggggacaagtaccccagacctggaacggcaggctc
potassium channel 274    T  L  T  T  I  G  Y  G  D  K  Y  P  Q  T  W  N  G  R  L

Query:          979  ggctgctggcttcgccttactgggcatctctttctttgccctgcctgccggcatccta
                     || ||  |||| || | | || |||| |||i| || ||||||||| ||||||| |
Sbjct:         1006  tgcggcaaccttcaccctcatcggtgtctccttcttcgcgctgcctgcaggcatcttg
potassium channel 294    A  A  T  F  T  L  I  G  V  S  F  F  A  L  P  A  G  I  L

Query:         1039  ctccggctttgccctgaaggtccaggagcagcaccggcagaagcacttcgagaagcgg
                     '| .| ||5:|||||||||| '||||||5:| || ||;||||||||| |||||| ||
Sbjct:         1066  gtctgggtttgccctgaaggttcaggagcagcacaggcagaagcactttgagaagagg
potassium channel 314    S  G  F  A  L  K  V  Q  E  Q  H  R  Q  K  H  F  E  K  R

Query:         1099  gatgccggcagccaacctcatccaggctgcctgg 1132
                     || |||||||| ||| ||| || | |||||i
Sbjct:         1126  gaacccggcagcaggcctgatccagtcggcctgg 1159
potassium channel 334    N  P  A  A  G  L  I  Q  S  A  W
```

Score = 150 bits (78), Expect = 5e-33
Identities = 124/147 (84%)
Strand = Plus / Plus

```
Query:             1705 gttcctggtggccaaaaggaaattcaaggagacactgcgaccgtacgacgtgaaggac
                        !!||||!|!| ||'|  !''| '!!| ||||||||||| '!|!' !' !!!!!!!!!! !!!!
Sbjct:             1768 gttcctggtgtccaagcggaagttcaaggagagcctgcggccctacgacgtgatggac
potassium channel 548    F  L  V  S  K  R  K  F  K  E  S  L  R  P  Y  D  V  M  D
```

```
Query:             1765 cattgagcagtactcagcaggccacctggacatgctgggccggatcaagagcctgcaa
                        !,! !!!!!!!,!!!!!,, '!'!!!!!!;!!!!!!!!!,·!  !!! !! !!!!!!!!!!!
Sbjct:             1828 catcgagcagtactcagccggccacctggacatgctgtcccgaattaagagcctgcag
potassium channel 568    I  E  Q  Y  S  A  G  H  L  D  M  L  S  R  I  K  S  L  Q
```

```
Query:             1825 tcgggtggaccaaattgtgggtcgggg 1851
                         !  ||'||!, |: !:||| |!'!|
Sbjct:             1888 cagagtggaccagatcgtggggcgggg 1914
potassium channel 588    R  V  D  Q  I  V  G  R  G
```

Score = 60.3 bits (31), Expect = 8e-06
Identities = 53/64 (82%)
 Strand = Plus / Plus

```
Query:             1921 cagcatgatgggacgcgtggtcaaggtggagaagcaggtgcagtccatcgagcacaag
                        !!!!!!!,!!!!!!!!! !! ! !!!!!!!!!!!;!!!!!  !!!!!! !!! ! !!!
Sbjct:             1978 cagcatgatgggacggctcgggaaggtggagaagcaggtcttgtccatggagaagaag
potassium channel 618    S  M  M  G  R  L  G  K  V  E  K  Q  V  L  S  M  E  K  K
```

```
Query:             1981 ggac 1984
                        !!||
Sbjct:             2038 ggac 2041
potassium channel 638    D
```

Score = 52.6 bits (27), Expect = 0.002
Identities = 41/48 (85%)
 Strand = Plus / Plus

```
Query:             1504 cagccccaccaaggtgcaaaagagctggagcttcaatgaccgcacccg 1551
                        !!|!|!!! !! !!'!! !!!!!!!!!!!!!!!!  !!!!!!! !!!
Sbjct:             1552 cagccccagcaaggtgcccaagagctggagcttcggggaccgcagccg 1599
potassium channel 476    S  P  S  K  V  P  K  S  W  S  F  G  D  R  S  R
```

CPU time: 0.12 user secs.   0.04 sys. secs   0.16 total secs.

Lambda   K   H
   1.33   0.621   1.12

Gapped
Lambda   K   H
   1.33   0.621   1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 21
Number of Sequences: 0
Number of extensions: 21

Number of successful extensions: 8
Number of sequences better than 10.0: 1
length of query: 2088
length of database: 5,708,689,566
effective HSP length: 25
effective length of query: 2063
effective length of database: 5,691,761,841
effective search space: 11742104677983
effective search space used: 11742104677983
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)